## SUPPLEMENTARY MATERIAL

**Supplementary Table S1.** Fatty acids selected to evaluate the effects on *C. elegans* fat content.

| Code | Common Name | CAS Number | MW[1] | Reference (supplier in superscript) ) |
|---|---|---|---|---|
| LAU | Dodecanoic acid (Lauric acid) | 143-07-7 | 200.32 | 10006626[2] |
| MIR | Tetradecanoic acid (Myristic acid) | 544-63-8 | 228.37 | M3128[3] |
| DHA | cis-4,7,10,13,16,19-docosahexaenoic acid | 6217-54-5 | 328.49 | 53171[3] U-84-A[4] |
| EPA | cis-5,8,11,14,17-eicosapentaenoic acid | 10417-94-4 | 302.45 | 44864[3] U-99-A[4] |
| ALA | cis-9,12,15-octadecatrienoic acid (Alpha-linolenic acid) | 463-40-1 | 278.43 | U-62-A[4] |
| SDA | cis-6,9,12,15-octadecatetraenoic acid (Stearidonic acid) | 20290-75-9 | 276.41 | 90320[2] |
| ETA | Eicosatrienoic acid | 1783-84-2 | 306.53 | U-70-A[4] |
| CPA | 9Z,11E,13E,15Z-octadecatetraenoic acid | 18427-44-6 | 276.41 | 71430[2] |
| ARA | cis-5,8,11,14-eicosatetraenoic acid (Arachidonic acid) | 24880-40-8 | 304.47 | 90011[2] |
| LA | cis-9,12-octadecadienoic acid (Linoleic acid) | 60-33-3 | 280.45 | L1376[3] U-59-A[4] |
| GLA | cis-6,9,12-octadecatrienoic acid (Gamma-linolenic acid) | 506-26-3 | 278.43 | L2378[3] U-63-A[4] |
| DGLA | cis-8,11,14-eicosatrienoic acid (Dihomo-gamma-linolenic acid) | 81540-86-5 | 306.53 | E4504[3] U-69-A[4] |
| PNA | cis-5,9,12-octadecatrienoic acid (Pinolenic acid) | 16833-54-8 | 278.43 | 10008654[2] |
| VCA | cis-11-octadecenoic acid (Vaccenic acid) | 506-17-2 | 282.46 | V0384[3] |
| ELA | 9-trans,11-trans-octadecadinoic acid | 544-71-8 | 280.45 | 90983[3] |
| ZLA | 9-cis,11-trans-octadecadinoic acid | 2540-56-9 | 280.45 | 16413[3] |
| POA | 9-cis-hexadecenoic acid (Palmitoleic acid) | 373-49-9 | 254.41 | P9417[3] |
| OLA | cis-9-octadecenoic acid (Oleic acid) | 112-80-1 | 282.46 | 75090[3] |
| ESA | cis-11-eicosenoic acid | 544-63-8 | 310.51 | E3635[3] |
| ERA | cis-13-docosenoic acid (Erucic acid) | 112-86-7 | 338.57 | 45629[3] |
| PSA | cis-6-octadecenoic acid | 593-39-5 | 282.46 | 10-1811-9[5] |

*[1]MW: Molecular weight (g/mol);.[2] Cayman Chemical Co., Ann Arbor, MI; [3] Sigma Aldrich Co., St. Louis, MO; [4] Nu-Chek Prep Inc., Elysian, MN; [5] Larodan AB, Solna, Sweden*

**Supplementary Table S2** Double-quenched probes for quantitative real-time PCR from IDT Technologies (Integrated DNA Technologies Inc., Coralville, IA). *Pmp-3* (Ce02485188_m1) and *tba-1* (Ce02412618_gH) Applied Biosystems™ TaqMan® Gene Expression Assays were used as housekeeping genes.

| Gene | Fluorophore | Quenchers | Sequences | (5' to 3') |
|---|---|---|---|---|
| *acox-1* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | AGCAAACTGGAAAGCGTAGG |
| | | | Primer 2 | AACAAGATACTCGGCAGTGAG |
| | | | Probe | CGGGCGATGAATGGGAAGAGACG |
| *maoc-1* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | CAGTAACCAATGTTTGTCCTGG |
| | | | Primer 2 | TCATGGATTGTGCAGTCTGG |
| | | | Probe | CTGCTTGGGCTGGAAATGATTCTGAC |
| *F58F9.7* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | ACTGGGATCTCATTTTCAGCG |
| | | | Primer 2 | GTTTGGGAACATTGTCAGTTGG |
| | | | Probe | CTCGGCGACAGTTTGGACCAGTAA |
| *daf-22* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | GGGATTTTGGATTGTGGACTG |
| | | | Primer 2 | CGGCTCAGATGTTTGGAAATG |
| | | | Probe | TGGTTCTTGTAGGCGATTTTGGCGT |
| *dhs-28* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | AAGTACACGGATGGAGATGC |
| | | | Primer 2 | GAAATGGCTGATGGTGTGAAG |
| | | | Probe | CACTGACGGAAAGAACGAGCTTGGA |
| *ech-3* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | CTGTTGAGGAGGCAGTGAAA |
| | | | Primer 2 | CTCCGTGTGTTCTAACGAGTAAT |
| | | | Probe | TCCGGAAATATGCATGCTGGCTGA |
| *acaa-2* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | CCTATTCTGCTGTCGGTTGT |
| | | | Primer 2 | CAATCTTGAGCCCACTCTTCT |
| | | | Probe | CGGCTCCAGCTATTCGGGAAGTTC |
| *B0303.3* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | TGACCACTGGAATGGGAATG |
| | | | Primer 2 | GAATTGGCACATCAGACAACAA |
| | | | Probe | ATGCAAATGCAATCATCGCCGGAG |
| *dif-1* | 6-FAM | ZEN™-Iowa Black® FQ | Primer 1 | CTGGAGAAGGAGCTCAAAGAAC |
| | | | Primer 2 | ACATCAGCTGGAATACACACTC |
| | | | Probe | TGGCTGGAGGACTTGCTGGTATTG |

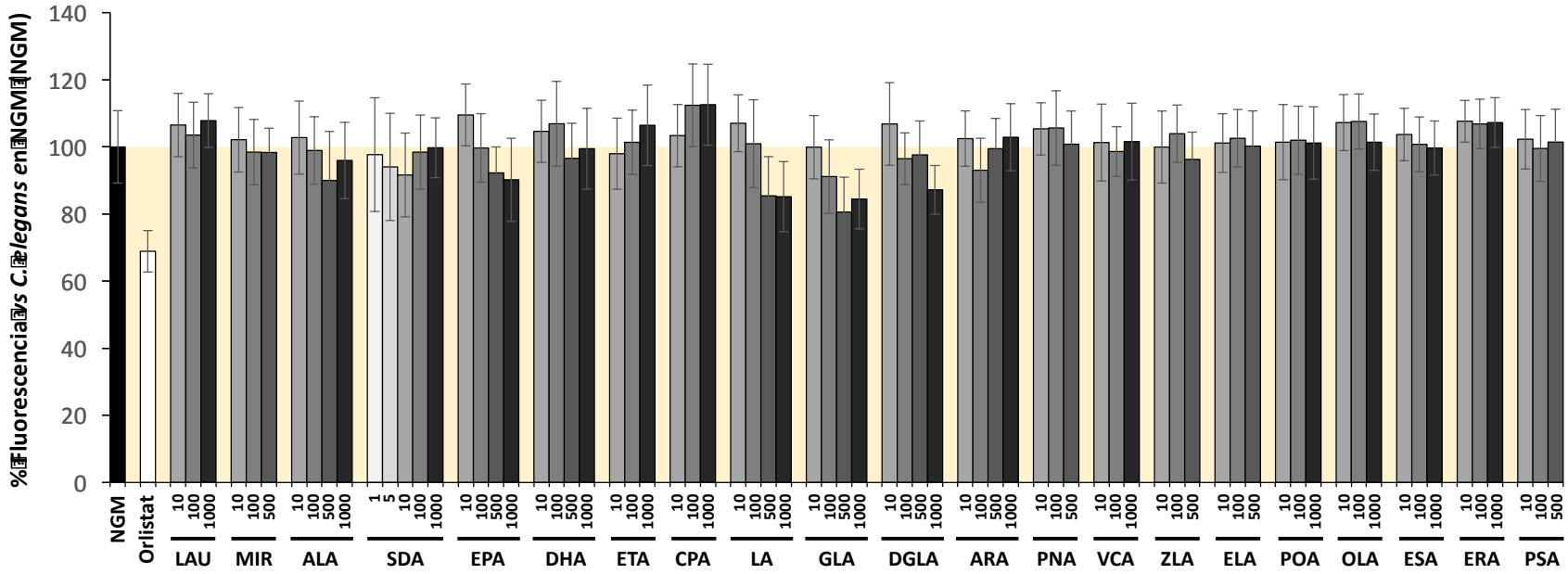
**Supplementary Table S3.** Microarray results: common altered genes ($p < 0.05$) among LA, GLA and DGLA-treated *vs* non-treated *C. elegans* (NGM). Fold change is shadowed in green for upregulated genes and in red for downregulated genes. Grey shadow in the Related Pathways column shows genes involved in FA ß-oxidation.

| Gene | ANOVA Fold Change (vs non-treated worms) | | | ANOVA p-value (vs non-treated worms) | | | Global *p*-value | Cellular Component | Related Pathways |
|---|---|---|---|---|---|---|---|---|---|
| | LNA | GLA | DGLA | LNA | GLA | DGLA | | | |
| *abhd-3.1* | 1.36 | 1.48 | 1.69 | 0.009466 | 1.07E-04 | 2.55E-04 | 2.58E-10 | plasma membrane | phosphatidylcholine biosynthetic process |
| *acdh-7* | 1.34 | 1.28 | 1.57 | 0.030737 | 0.013607 | 0.028396 | 1.19E-05 | mitochondrion | fatty acid beta-oxidation / metabolic process / fatty acid beta-oxidation using acyl-CoA dehydrogenase / lipid homeostasis / oxidation-reduction process |
| *acl-5* | 1.41 | 1.27 | 1.23 | 0.004446 | 0.010553 | 0.022048 | 1.03E-06 | endoplasmic reticulum | lipid biosynthetic process / metabolic process |
| *acox-1* | 1.59 | 2.05 | 2.22 | 1.60E-04 | 4.34E-04 | 5.70E-05 | 3.96E-12 | peroxisome | fatty acid beta-oxidation / fatty acid metabolic process / metabolic process / fatty acid beta-oxidation using acyl-CoA dehydrogenase / lipid homeostasis / oxidation-reduction process / ascaroside biosynthetic process |
| *acs-14* | 1.32 | 1.36 | 1.48 | 0.007796 | 0.016832 | 0.007164 | 9.40E-07 | mitochondrion | fatty acid beta-oxidation / Long-chain fatty-acyl-CoA biosynthetic process / metabolic process |
| *acs-5* | 1.14 | 1.29 | 1.4 | 0.011958 | 0.025067 | 0.008244 | 2.47E-06 | peroxisome / mitochondrion | fatty acid beta-oxidation / fatty acid transport / metabolic process / determination of adult lifespan / lipid storage |
| *acs-7* | 1.73 | 2.12 | 1.95 | 0.001262 | 7.70E-04 | 9.64E-04 | 9.37E-10 | mitochondrion | fatty acid beta-oxidation / Long-chain fatty-acyl-CoA biosynthetic process / metabolic process |
| *alh-10* | 1.39 | 1.24 | 1.33 | 0.008156 | 0.002855 | 0.003069 | 7.15E-08 | cytoplasm | retinoic acid metabolic process / metabolic process / multicellular organism homeostasis / oxidation-reduction process |
| *asp-10* | 1.45 | 1.4 | 1.3 | 0.002414 | 0.004885 | 0.013389 | 1.58E-07 | endosome | protein catabolic process / proteolysis |
| *asp-13* | 1.7 | 1.29 | 1.19 | 0.001415 | 0.00952 | 0.022767 | 3.07E-07 | extracellular space | protein catabolic process / proteolysis |
| *ast-1* | 1.18 | 1.25 | 1.32 | 0.021276 | 0.013423 | 0.026687 | 7.62E-06 | nucleus | positive regulation of transcription from RNA polymerase II promoter / nematode larval development / regulation of transcription, DNA-templated / embryo development ending in birth or egg hatching / oviposition / dopaminergic neuron differentiation |
| *B0272.3* | 1.4 | 1.36 | 1.37 | 0.010859 | 0.001625 | 0.003118 | 5.50E-08 | mitochondrion | fatty acid beta-oxidation / lipid metabolic process / fatty acid metabolic process / oxidation-reduction process |
| *B0272.4* | 1.8 | 2.46 | 2.95 | 0.007615 | 0.001132 | 1.61E-04 | 1.39E-09 | peroxisome | fatty acid beta-oxidation / metabolic process |
| *B0303.3* | 1.19 | 1.22 | 1.23 | 0.032082 | 0.020181 | 0.03255 | 2.11E-05 | mitochondrion | fatty acid beta-oxidation / metabolic process / embryo development ending in birth or egg hatching |
| *C16D9.1* | 1.47 | 1.38 | 1.54 | 0.047139 | 0.004638 | 0.048018 | 1.05E-05 | | epithelial cell development / molting cycle process / cuticle development |
| *C23H4.6* | -1.1 | -1.07 | -1.08 | 0.005561 | 0.03614 | 0.00654 | 1.31E-06 | nucleus | structural maintenance of chromosomes / double-strand break repair via homologous recombination / DNA repair / resolution of recombination intermediates |
| *clec-174* | -2.32 | -1.97 | -4.2 | 0.00335 | 0.005329 | 1.75E-04 | 3.12E-09 | | O-glycan processing / defense response / innate immune response |
| *clec-49* | 1.49 | 1.26 | 1.29 | 0.017912 | 0.006313 | 0.038927 | 4.40E-06 | | |
| *cpr-5* | 1.11 | 1.12 | 1.1 | 3.96E-04 | 0.002104 | 0.01505 | 1.25E-08 | lysosome | proteolysis / proteolysis involved in cellular protein catabolic process |
| *cpt-4* | -2.1 | -1.62 | 1.54 | 1.40E-05 | 5.31E-04 | 4.00E-05 | 2.97E-13 | mitochondrion | fatty acid beta-oxidation |
| *cyp-35A3* | -1.86 | -2.71 | -1.82 | 9.80E-04 | 6.65E-04 | 0.020004 | 1.30E-08 | endoplasmic reticulum | lipid storage / response to xenobiotic stimulus / oxidation-reduction process |
| *D2063.1* | 1.65 | 1.71 | 1.5 | 0.00854 | 0.003237 | 0.009474 | 2.62E-07 | | oxidation-reduction process / ethanol oxidation |
| *daf-22* | 1.41 | 1.82 | 2.08 | 0.017833 | 0.001344 | 6.03E-04 | 1.45E-08 | peroxisome | fatty acid beta-oxidation / very long-chain fatty acid metabolic process / acyl-CoA metabolic process / steroid biosynthetic process / transport / lipid transport / metabolic process / dauer larval development / lipid storage / response to pheromone / lipid storage / cholesterol transport / positive regulation of intracellular cholesterol transport / pheromone biosynthetic process / dauer entry / dauer exit / positive regulation of developmental growth / regulation of chemotaxis / positive regulation of nematode larval development / ascaroside biosynthetic process |
| *dhs-19* | 1.53 | 1.8 | 1.32 | 0.046095 | 9.10E-05 | 0.002841 | 1.19E-08 | endoplasmic reticulum | retinol metabolic proces |
| *dhs-28* | 1.35 | 1.52 | 1.71 | 0.00199 | 2.36E-04 | 3.13E-04 | 1.47E-10 | peroxisome | fatty acid beta-oxidation / very long-chain fatty acid metabolic process / acyl-CoA metabolic process / negative regulation of lipid storage / response to pheromone / lipid storage / response to food / response to starvation / pheromone biosynthetic process / dauer entry / positive regulation of developmental growth / oxidation-reduction process / positive regulation of nematode larval development / ascaroside biosynthetic process |
| *dif-1* | 1.24 | 1.22 | 1.45 | 0.018925 | 0.001614 | 0.002063 | 6.30E-08 | mitochondrion | fatty acid beta-oxidation / acyl carnitine transmembrane transport / translation / transport / mitochondrial transport / multicellular organism development / embryo development ending in birth or egg hatching / transmembrane transport |
| *ech-8* | 2 | 1.93 | 2.64 | 0.007927 | 0.00512 | 0.001683 | 6.83E-08 | peroxisome | fatty acid beta-oxidation / fatty acid metabolic process / lipid storage / oxidation-reduction process |
| *F13B9.2* | 1.54 | 1.35 | 1.36 | 0.001511 | 0.004778 | 0.002773 | 2.00E-08 | | |
| *F17C11.6* | 1.44 | 1.27 | 1.28 | 0.02202 | 0.017683 | 0.018758 | 7.30E-06 | | |
| *F31D4.8* | 1.37 | 1.29 | 1.29 | 0.012061 | 0.001553 | 0.001721 | 3.22E-08 | | |
| *F35E12.5* | -2.33 | -2.78 | -9.02 | 0.017006 | 6.77E-04 | 1.01E-04 | 1.16E-09 | | innate immune response / defense response to Gram-negative bacterium |
| *F46B6.6* | 1.26 | 1.21 | 1.21 | 0.015086 | 0.022562 | 0.025198 | 8.58E-06 | mitochondrion | mitochondrial translational initiation / receptor-mediated endocytosis |
| *F53C11.3* | 1.69 | 2.27 | 2.76 | 0.001423 | 9.00E-06 | 6.50E-05 | 8.32E-13 | mitochondrion | fatty acid beta-oxidation / lipid storage / innate immune response / defense response to Gram-negative bacterium / oxidation-reduction process |
| *F57G12.1* | 1.16 | 1.17 | 1.17 | 0.026737 | 0.010008 | 0.020463 | 5.48E-06 | | |
| *F58A6.1* | 1.35 | 1.46 | 1.72 | 2.80E-04 | 8.18E-04 | 0.01071 | 2.45E-09 | peroxisome / mitochondrion | fatty acid beta-oxidation / metabolic process / fatty acid catabolic process |
| *F58F9.7* | 1.28 | 1.81 | 1.91 | 0.005118 | 2.41E-04 | 0.002743 | 3.38E-09 | peroxisome | fatty acid beta-oxidation / fatty acid metabolic process / metabolic process / fatty acid beta-oxidation using acyl-CoA dehydrogenase / lipid homeostasis / oxidation-reduction process |
| *far-3* | 6.61 | 30.56 | 30.32 | 0.001142 | 2.00E-06 | 3.00E-06 | 6.85E-15 | | |
| *fat-5* | 4.65 | 2.51 | 2.86 | 4.22E-04 | 0.002457 | 0.001026 | 1.06E-09 | endoplasmic reticulum | long-chain fatty-acyl-CoA biosynthetic process / lipid metabolic process / fatty acid metabolic process / fatty acid biosynthetic process / unsaturated fatty acid biosynthetic process / multicellular organism development / positive regulation of multicellular organism growth / oxidation-reduction process |
| *fipr-2* | 1.19 | 1.28 | 1.49 | 0.042053 | 0.010355 | 0.006176 | 2.69E-06 | | |
| *gba-1* | 1.13 | 1.08 | 1.12 | 0.044599 | 0.024042 | 0.013929 | 1.49E-05 | lysosome | lipid metabolic process / carbohydrate metabolic process / sphingolipid metabolic process |
| *glo-3* | -1.11 | -1.12 | -1.13 | 0.009572 | 0.013644 | 0.034879 | 4.56E-06 | | reproduction / apoptotic process / embryo development ending in birth or egg hatching / 3'-UTR-mediated mRNA destabilization |
| *hacd-1* | -2.4 | -2.4 | -1.58 | 0.001397 | 0.002867 | 0.01077 | 4.31E-08 | mitochondrion | fatty acid beta-oxidation / fatty acid metabolic process / oxidation-reduction process |
| *irg-3* | 3.95 | 6.23 | 6.36 | 7.98E-04 | 1.60E-05 | 2.70E-05 | 3.45E-13 | | innate immune response |
| *K04B12.2* | 1.17 | 1.07 | 1.04 | 0.04954 | 0.021702 | 0.037901 | 4.07E-05 | | |
| *K09H11.1* | 1.91 | 2.59 | 2.89 | 8.37E-04 | 4.30E-05 | 2.10E-05 | 7.56E-13 | mitochondrion | fatty acid beta-oxidation / metabolic process / fatty acid beta-oxidation using acyl-CoA dehydrogenase / lipid homeostasis / oxidation-reduction process |
| *lem-3* | -1.12 | -1.26 | -1.21 | 0.048553 | 1.67E-04 | 4.71E-04 | 3.82E-09 | | reproduction / DNA catabolic process, endonucleolytic / cellular response to DNA damage stimulus / axonal fasciculation / response to UV / embryo development ending in birth or egg hatching / response to X-ray / response to UV-C / dendrite development |
| *lys-4* | 1.72 | 1.43 | 1.62 | 0.001242 | 3.43E-04 | 1.80E-05 | 7.67E-12 | | carbohydrate metabolic process / peptidoglycan catabolic process / cell wall macromolecule catabolic process |
| *maoc-1* | 1.4 | 1.78 | 2.32 | 0.014091 | 3.08E-04 | 3.48E-04 | 1.51E-09 | peroxisome | fatty acid beta-oxidation / determination of adult lifespan / lipid storage / innate immune response / defense response to Gram-negative bacterium |
| *msra-1* | 1.29 | 1.18 | 1.34 | 0.007517 | 0.02389 | 0.002734 | 4.91E-07 | | response to oxidative stress / protein repair / oxidation-reduction process |
| *mtrr-1* | 1.15 | 1.21 | 1.14 | 0.019429 | 0.023949 | 0.024722 | 1.15E-05 | cytoplasm | cellular amino acid biosynthetic process / oxidation-reduction process |
| *ncr-1* | -1.23 | -1.16 | -1.32 | 0.031153 | 0.005679 | 0.001911 | 3.38E-07 | plasma membrane | multicellular organism development / embryo development ending in birth or egg hatching / cholesterol transport / positive regulation of growth rate / dauer larval development / cholesterol homeostasis / regulation of oviposition |
| *nhr-11* | 1.79 | 1.91 | 2.43 | 0.039685 | 0.006082 | 0.002873 | 6.93E-07 | nucleus | lipid metabolic process / transcription, DNA-templated / regulation of transcription, DNA-templated / steroid hormone mediated signaling pathway |
| *nhr-49* | 1.1 | 1.09 | 1.11 | 0.013274 | 0.019746 | 0.011609 | 3.04E-06 | | lipid storage / reproduction / nematode larval development / transcription, DNA-templated / regulation of transcription, DNA-templated / receptor-mediated endocytosis / determination of adult lifespan / embryo development ending in birth or egg hatching / gene expression / regulation of lipid metabolic process / regulation of fatty acid metabolic process / positive regulation of transcription from RNA polymerase II promoter in response to stress / locomotion / steroid hormone mediated signaling pathway / positive regulation of transcription from RNA polymerase II promoter |
| *npp-5* | 1.1 | 1.06 | 1.05 | 0.015583 | 0.004485 | 0.041024 | 2.87E-06 | | posttranscriptional tethering of RNA polymerase II gene DNA at nuclear periphery / regulation of transcription, DNA-templated / mRNA export from nucleus / protein import into nucleus / transport / embryo development ending in birth or egg hatching |
| *pho-6* | 1.35 | 1.42 | 1.7 | 0.016019 | 0.013239 | 0.012901 | 2.74E-06 | lysosome | dephosphorylation |
| *prx-12* | 1.34 | 1.29 | 1.35 | 0.02374 | 0.031022 | 0.049358 | 3.64E-05 | peroxisome | peroxisome organization / protein targeting to peroxisome / nematode larval development / protein monoubiquitination / transport / embryo development ending in birth or egg hatching / protein transport / protein import into peroxisome matrix |
| *prx-3* | 1.31 | 1.24 | 1.46 | 0.015159 | 0.010922 | 0.009607 | 1.59E-06 | peroxisome | peroxisome organization / protein import into peroxisome membrane |
| *R05G6.9* | 1.22 | 1.15 | 1.2 | 0.02456 | 0.009748 | 0.014022 | 3.36E-06 | | Development |
| *R07A4.2* | 1.28 | 1.18 | 1.41 | 7.50E-04 | 0.003752 | 0.006821 | 1.92E-08 | | lipid storage |
| *scpl-1* | 1.11 | 1.09 | 1.09 | 0.005549 | 0.023041 | 0.014482 | 1.85E-06 | nucleus | protein dephosphorylation / dephosphorylation / oviposition / regulation of oviposition |
| *ssq-2* | -1.2 | -1.18 | -1.2 | 3.04E-04 | 0.004527 | 6.10E-05 | 8.39E-11 | | locomotion |
| *swt-6* | -1.2 | -1.23 | -1.28 | 0.044878 | 0.006626 | 0.007797 | 2.32E-06 | plasma membrane | carbohydrate transmembrane transport |
| *T16G12.8* | -1.07 | -1.18 | -1.07 | 0.040383 | 0.02832 | 4.72E-02 | 5.40E-05 | | |
| *T22F7.4* | 1.63 | 1.25 | 1.18 | 0.00647 | 0.041163 | 0.033478 | 8.92E-06 | | |
| *T24B8.5* | -1.45 | -1.81 | -1.82 | 0.008042 | 0.001606 | 0.003103 | 4.01E-08 | | innate immune response |
| *T27F6.8* | -1.18 | -1.15 | -1.2 | 0.035878 | 0.024067 | 0.00709 | 6.12E-06 | | |
| *tag-10* | 1.22 | 1.22 | 1.41 | 0.001913 | 0.00192 | 0.0044 | 1.62E-08 | | |
| *ugt-22* | -1.13 | -1.17 | -1.19 | 8.00E-04 | 0.001561 | 0.031928 | 3.99E-08 | endoplasmic reticulum | flavonoid biosynthetic process / retinoic acid metabolic process / fatty acid metabolic process / metabolic process / flavonoid glucuronidation |
| *W01A11.1* | 1.15 | 1.31 | 1.42 | 0.038845 | 0.00137 | 0.001594 | 8.48E-08 | endoplasmic reticulum | response to toxic substance |
| *Y23H5B.8* | 1.43 | 1.19 | 1.41 | 8.27E-04 | 0.031704 | 0.001298 | 3.40E-08 | | |
| *Y25C1A.13* | 1.25 | 1.46 | 1.82 | 0.007054 | 0.010306 | 0.001712 | 1.24E-07 | peroxisome / mitochondrion | fatty acid beta-oxidation / nematode larval development / metabolic process / fatty acid catabolic process |
| *Y32F6B.1* | 1.26 | 1.15 | 1.51 | 0.025085 | 0.01124 | 3.20E-04 | 9.02E-08 | plasma membrane | prostaglandin transport / transport / ion transport / sodium-independent organic anion transport |
| *Y38E10A.14* | 1.31 | 1.33 | 1.65 | 0.002761 | 5.75E-04 | 3.85E-04 | 6.11E-10 | | |
| *Y42A5A.3* | -1.32 | -1.36 | -1.34 | 0.009202 | 0.004179 | 0.02966 | 1.14E-06 | | |
| *Y47D3A.5* | -1.27 | -1.14 | -1.17 | 0.017148 | 0.013399 | 0.00508 | 1.17E-06 | | |
| *Y53G8B.2* | 1.59 | 1.55 | 1.81 | 0.007828 | 0.004743 | 0.002666 | 9.90E-08 | endoplasmic reticulum | triglyceride biosynthetic process |
| *Y54G11A.7* | 1.54 | 1.51 | 1.58 | 0.010974 | 0.043828 | 0.01656 | 7.96E-06 | | embryo development ending in birth or egg hatching |
| *Y87G2A.2* | 1.91 | 2.73 | 3.18 | 0.006842 | 4.60E-05 | 2.63E-04 | 8.28E-11 | peroxisome | fatty acid beta-oxidation / acyl-CoA metabolic process / growth |
| *zip-5* | -1.6 | -1.47 | -1.4 | 0.035188 | 0.018526 | 0.029434 | 1.92E-05 | | regulation of transcription from RNA polymerase II promoter / regulation of transcription, DNA-templated |
| *ZK593.3* | 1.53 | 1.32 | 1.41 | 0.006875 | 0.021385 | 0.011455 | 1.68E-06 | | lipid storage |

**Supplementary Figure S1. Results of the effect of the 21 selected FAs on fat content in *C. elegans* N2.**

The graph shows the percentage (± standard deviation) of the mean fluorescence of N2 L4 worms treated with increasing concentrations of each FA *vs* non-treated N2 worms (NGM: black bars). The positive control, Orlistat (ORL)-treated worms (6 µg/mL), is represented with a white bar. For all fatty acids, 1, 5, 10, 100, 500 and 1000 reflect treatment concentrations (µM) in the X-axis. For LAU, ETA, CPA, VCA, POA, ESA and ERA supplementations, three experiments at 10, 100, and 1000 µM each were performed. For OLA, four assays at concentrations of 10, 100, and 1000 µM each were performed. For DHA, EPA, ALA, LA, GLA, DGLA and ARA six assays were carried out at concentrations of 10, 100, 500 and 1000 µM; and the same number of assays for SDA but at concentrations of 1, 5, 10, 100 and 1000 µM. As each assay was performed at the same time with a positive (ORL) and a negative (NGM) controls, data from ORL and NGM columns represent the results from 11 different experiments.

Light yellow pattern represents the mean fluorescence (considered as 100%) observed in the non-treated (NGM) worms, included for easier comparison.


%Fluorescencia vs C.elegans en NGM (NGM)
140
120
100
80
60
40
20
0
NGM
Orlistat
LAU
MIR
ALA
SDA
EPA
DHA
ETA
CPA
LA
GLA
DGLA
ARA
PNA
VCA
ZLA
ELA
POA
OLA
ESA
ERA
PSA

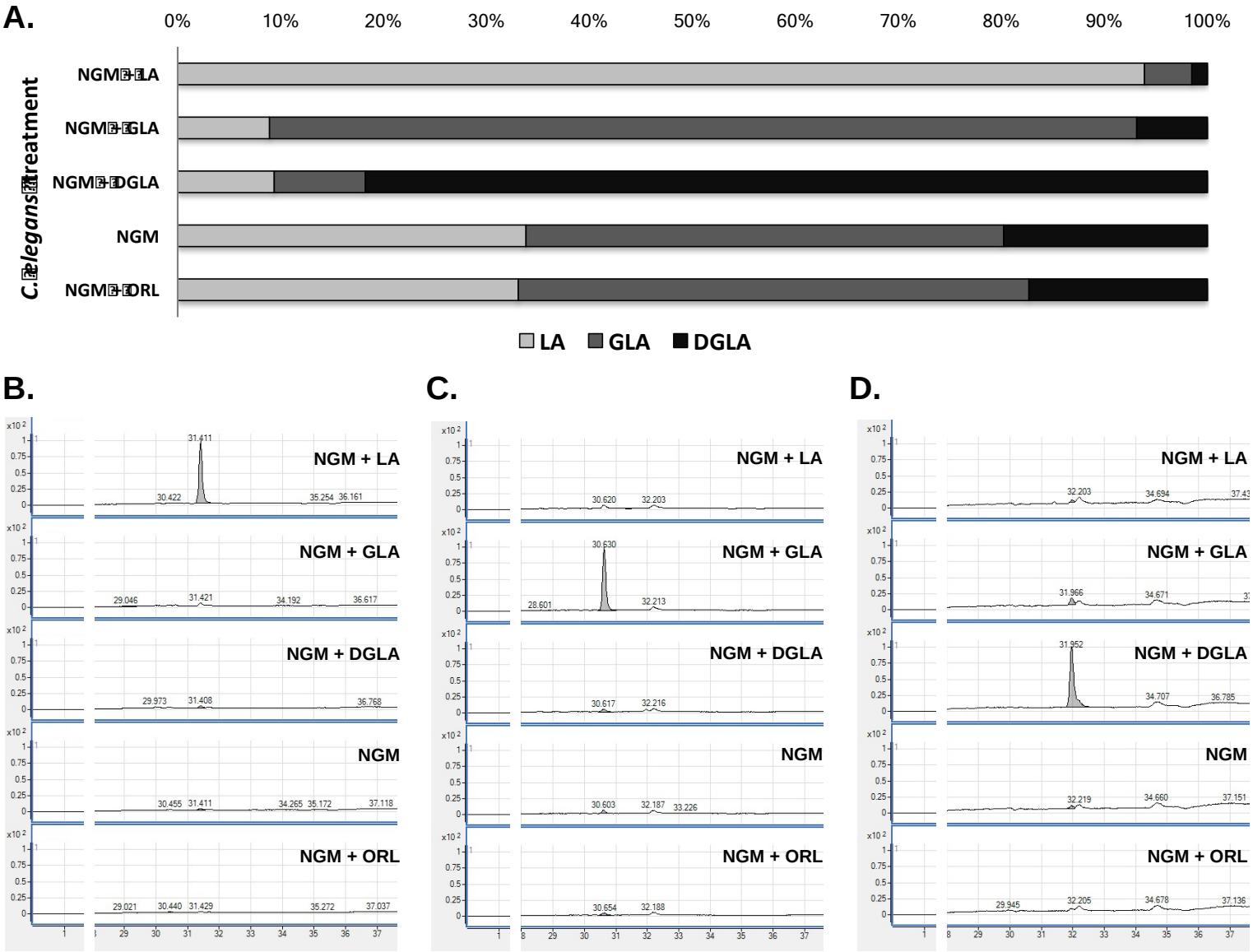
**Supplementary Figure S2. Determination of Fatty acid uptake by Accurate-Mass TOF LC/MS.**

**A. LA:GLA:DGLA ratio in worms grown in supplemented media.** The graph shows the ratio of LA, GLA and DGLA inside the worms grown in each media (calculated as percentage of each individual FA quantified by Accurate-Mass TOF LC/MS related to the total amount of LA, GLA and DGLA, quantified by Accurate-Mass TOF LC/MS). NGM + LA: NGM supplemented with 1000 µM of LA; NGM + GLA: NGM supplemented with 1000 µM of GLA; NGM + DGLA: NGM supplemented with 1000 µM of DGLA; NGM: Nematode Growth Medium; NGM + Orlistat: NGM supplemented with 6 µg/mL of Orlistat.

**B. Extracted Ion Chromatogram for LA m/z of extracted lipids from worms grown in different supplemented media.** NGM + LA: NGM supplemented with 1000 µM of LA; NGM + GLA: NGM supplemented with 1000 µM of GLA; NGM + DGLA: NGM supplemented with 1000 µM of DGLA; NGM: Nematode Growth Medium; NGM + Orlistat: NGM supplemented with 6 µg/mL of Orlistat.

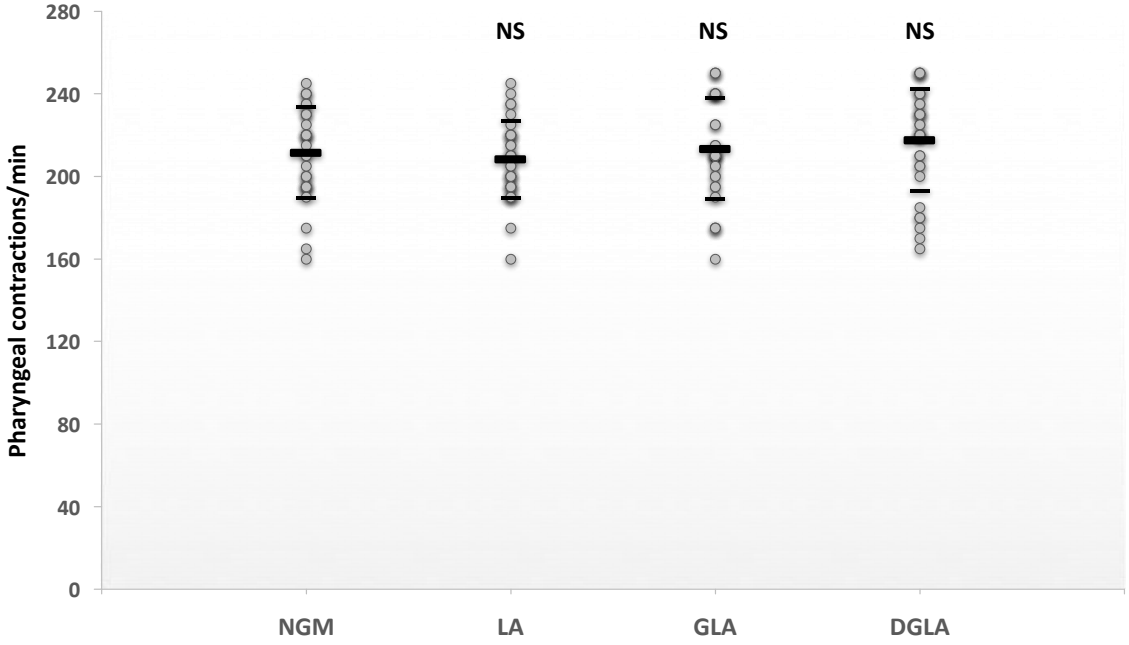
**C. Extracted Ion Chromatogram for GLA m/z of extracted lipids from worms grown in different supplemented media.** NGM + LA: NGM supplemented with 1000 µM of LA; NGM + GLA: NGM supplemented with 1000 µM of GLA; NGM + DGLA: NGM supplemented with 1000 µM of DGLA; NGM: Nematode Growth Medium; NGM + Orlistat: NGM supplemented with 6 µg/mL of Orlistat.

**D. Extracted Ion Chromatogram for DGLA m/z of extracted lipids from worms grown in different supplemented media.** NGM + LA: NGM supplemented with 1000 µM of LA; NGM + GLA: NGM supplemented with 1000 µM of GLA; NGM + DGLA: NGM supplemented with 1000 µM of DGLA; NGM: Nematode Growth Medium; NGM + Orlistat: NGM supplemented with 6 µg/mL of Orlistat.


A.
0%
10%
20%
30%
40%
50%
60%
70%
80%
90%
100%
C. elegans treatment
NGM + LA
NGM + GLA
NGM + DGLA
NGM
NGM + ORL
LA
GLA
DGLA
B.
C.
D.
31.411
30.422
35.254
36.161
29.046
31.421
34.192
36.617
29.973
31.408
36.768
30.455
31.411
34.265
35.172
37.118
29.021
30.440
31.429
35.272
37.037
30.620
32.203
30.630
28.601
32.213
30.617
32.216
30.603
32.187
33.226
30.654
32.188
32.203
34.694
31.966
34.671
31.952
34.707
36.785
32.219
34.660
37.151
29.945
32.205
34.678
37.136

**Supplementary Figure S3. Pharyngeal pumping rate of wild-type worms treated with LA, GLA and DGLA.**

The graph displays the number of contractions of the pharyngeal bulb of worms, grown in the different conditions, per min (FC/min). Grey dots represent individual data for each condition; horizontal lines represent the mean of FC of each group (thick lines) and the mean ± one standard deviation of the mean values (thin lines). NGM: non-treated N2 worms; LA: 1000 µM LA-treated N2 worms; GLA: 1000 µM GLA-treated N2 worms; DGLA: 1000 µM DGLA-treated N2 worms. NS is non-significant differences.



**Supplementary Figure S4. Effect size analysis of N2 and *maoc-1* mutant strains.**

The graph displays the Cohen's *d* (the difference between group means of the treated and untreated worms divided by the combined standard deviation) of linoleic acid (LA), gamma-linoleic acid (GLA) and dihomo-gamma-linolenic acid (DGLA) effect on N2 and *maoc-1* strains. According to the standard scale there is no effect when $d \leq 0.2$, there is a small effect when $d \geq 0.2$, there is a medium effect when $d \geq 0.5$ and there is a large effect when $d \geq 0.8$.